

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2003, 16:23:48 ; Search time 40.4571 Seconds
(without alignments)
102.055 Million cell updates/sec

Title: US-09-905-691-5

Perfect score: 16

Sequence: 1 CRRARAARARAE 16

Scoring table:

Gapop 60.0 , Gapert 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	56.2	105	2 P96802	P96802 mycobacteri
2	9	56.2	105	16 Q9CCQ8	Q9CCQ8 mycobacteri
3	9	56.2	190	16 P71658	P71658 mycobacteri
4	9	56.2	406	10 Q94EV7	Q94EV7 zea mays (m
5	9	56.2	750	16 Q9KXP6	Q9KXP6 streptomyce
6	8	50.0	101	11 Q8BMV6	Q8BMV6 mus musculu
7	8	50.0	167	10 Q8S1J9	Q8S1J9 oryza sativ
8	8	50.0	200	2 Q9X696	Q9X696 streptomyce
9	8	50.0	204	12 Q85545	Q85545 bovine herp
10	8	50.0	274	10 Q8G2E4	Q8G2E4 pyrocystis
11	8	50.0	336	2 Q9X4X0	Q9X4X0 pseudomonas
12	8	50.0	356	7 Q31191	Q31191 mus musculu
13	8	50.0	383	16 Q314A1	Q314A1 pseudomonas
14	8	50.0	451	10 Q8S1I2	Q8S1I2 oryza sativ
15	8	50.0	710	16 Q8YER0	Q8YER0 brucella me
16	8	50.0	820	16 Q98C41	Q98C41 rhizobium l

RESULT 1

P96802 PRELIMINARY; PRT; 105 AA.
AC P96802;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Integration host factor.
GN MIHF.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RA Pedulla M.L., Lee M.H., Lever D.C., Hatfull G.F.;
RT "A novel host factor for integration of mycobacteriophage L5.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75344; AAC28246.1; -;
SQ SEQUENCE 105 AA; 11635 MW; B73846DBFA6CA838 CRC64;

Query Match 56.2%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15

Db 19 AAARRARAE 27

RESULT 2

Q9CCQ8 PRELIMINARY; PRT; 105 AA.
AC Q9CCQ8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Putative integration host factor.
GN MIHF OR ML0540.

060961 leishmania
Q92K3 streptomyce
Q8YUB7 anabaena sp
Q8368 salmonella
Q8fj3 escherichia
O11376 molluscum c
Q98316 molluscum c
Q8286 ananas como
Q8XB54 chlorobium
Q8n9d2 homo sapien
Q910c1 pseudomonas
Q8nh35 homo sapien
Q93r0 caulobacter
Q8nh12 oryza sativ
Q8f832 corynebacte
Q9f6m4 agrobacteri
Q8WY44 homo sapien
Q9u5w9 manduca sex
Q8Kq0 xanthomonas
Q9d6j8 mus musculus
O11344 molluscum c
Q8prf8 xanthomonas
Q8xj0 raietonia s
Q8fwq1 brucella su
Q8s6w0 oryza sativ
Q8Ym6 brucella me
Q94j70 oryza sativ
Q8nrm1 corynebacte

ALIGNMENTS

OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 DR EMBL; AL583918; CAC30048.1; -.
 DR Lepronia; ML0540; -.
 KW Complete proteome.
 SQ SEQUENCE 105 AA; 11506 MW; BDCD218AEFF76238 CRC64;

Query Match 56.2%; Score 9; DB 16; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15
 Db | | | | | | | | | |
 19 AAARRARAE 27

RESULT 3

ID P71658 PRELIMINARY; PRT; 190 AA.
 AC P71658;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein RV1388.
 GN RV1388 OR M71433 OR M7C21B4.05.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO M.SMEGMATIS MIHF.

DR EMBL; Z80108; CAB02193.1; -.
 DR EMBL; AE007015; AKA45698.1; ALT_INIT.
 DR TIGR; M71433; -.
 DR TubercuList; RV1388; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 190 AA; 20835 MW; 376672DCF96AF60D CRC64;

Query Match 56.2%; Score 9; DB 16; Length 190;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15
 Db | | | | | | | | | |
 104 AAARRARAE 112

RESULT 4

ID Q94EV7 PRELIMINARY; PRT; 406 AA.
 AC Q94EV7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE MAP kinase kinase.
 GN MAPKK1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-Huck1;
 RA Fu H., Zheng Z., Dooner H.K.;
 RT "Large differences in recombination rates within adjacent gene-dense
 and retrotransposon regions of maize";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF391808; AAK73104.1; -.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002965; P-rich_extensn.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR01217; PRICHEXTENS.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 406 AA; 44664 MW; DBFIDE6368F47DF0 CRC64;

Query Match 56.2%; Score 9; DB 10; Length 406;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAARAAR 10
 Db | | | | | | | | | |
 72 RRAARAAR 80

RESULT 5

ID Q9KXP6 PRELIMINARY; PRT; 750 AA.
 AC Q9KXP6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO1504.
 GN SCO1504 OR SC9C5.28.
 OS Streptomyces coelicolor.

Sat Aug 9 19:18:32 2003

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;

RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2);

RA Brown S.P., Harris D.;
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2);

RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2);

RA Redenbach M., Kleser H.M., Denapalte D., Elchner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;

RA "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).

RN SEQUENCE FROM N.A.
 RP STRAIN-A3(2)/M145;

RA MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rabbinkowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;

RA "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).

DR EMBL; AL939109; CAB93384.1; -
 DR InterPro; IPR000767; Disease_Resist.

DR PRINTS; PR00364; DISEASERESIST.
 DR Hypothetical protein; Complete proteome.

KW Hypothetical type I antifreeze protein containing protein
 SQ SEQUENCE 750 AA; 81839 MW; 469E5F417EDC8862 CRC64;

Query Match 56.28; Score 9; DB 16; Length 750;
 Best Local Similarity 100.0%; Pred. No. 14; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 AAAAAA 12

DB 76 AAAAAA 84

RESULT 6

Q8BMV6 PRELIMINARY; PRT; 101 AA.

AC Q8BMV6;

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)

DE Hypothetical type I antifreeze protein containing protein
 DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J; TISSUE=Eye;

RX MEDLINE=22354683; PubMed=12466851;

RA THE FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK021392; BAC25654.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 101 AA; 10110 MW; C8DCDC2D530ABB15 CRC64;

Query Match 50.08; Score 8; DB 11; Length 101;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RAARAAAR 10

DB 67 RAARAAAR 74

RESULT 7

Q8SLJ9 PRELIMINARY; PRT; 167 AA.

AC Q8SLJ9;

DT 01-JUN-2002 (TREMELrel. 21, Created)

DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE P0684C02.19 protein.

GN P0684C02.19.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
 RT clone: P0684C02.19";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP003290; BAB89063.1; -

DR Gramene; Q8SLJ9; -

SQ SEQUENCE 167 AA; 18542 MW; 0C40040DFB49021B CRC64;

Query Match 50.08; Score 8; DB 10; Length 167;
 Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRAARAAA 9

DB 20 RRAARAAA 27

RESULT 8

Q9X696 PRELIMINARY; PRT; 200 AA.

AC Q9X696;

DT 01-NOV-1999 (TREMELrel. 12, Created)

DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)

DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)

DE Vdcb.

GN VDCB.

OS Streptomyces sp. (strain D7).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=92742;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-D7;

RX MEDLINE=99445180; PubMed=10517592;
 RA Chow K.T., Pope M.K., Davies J.;

RT "Characterization of a vanillic acid non-oxidative decarboxylation
 RL gene cluster from Streptomyces sp. D7.";
 RL Microbiology 145:2393-2403(1999).
 DR EMBL; AF134589; AAD28781.1; -
 DR InterPro; IPR003382; Flavoprotein.

DR InterPro: IPR004507; Ublx.
DR Pfam: PF02441; Flavoprotein: 1.
DR TIGRFAMs: TIGR00421; ublx: 1.
SQ SEQUENCE 200 AA; 21660 MW; 83D1B5C22C13CD3E CRC64;

Query Match 50.0%; Score 8; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
Db 187 RAARAAAR 194

RESULT 9
Q65545 PRELIMINARY; PRT; 204 AA.
AC Q65545;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE UL3 protein.
GN UL3.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cooper;
RX MEDLINE=96036477; PubMed=7483276;
RA Khattar S.K., van Drunen Littel-van den Hurk S., Babiuk L.A.,
RA Tikoo S.K.;
RT Identification and transcriptional analysis of a 3'-coterminal gene
RT cluster containing UL1, UL2, UL3, and UL3.5 open reading frames of
RT bovine herpesvirus-1.;
RL Virology 213:28-37(1995).
DR EMBL; U32173; AAC54557.1;
DR InterPro: IPR005035; Herpes_UL3.
DR InterPro: IPR005829; Sug. transporter..
DR Pfam; PF03369; Herpes_UL3; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
SQ SEQUENCE 204 AA; 21792 MW; 9292E6A8AA2CB8C6 CRC64;

Query Match 50.0%; Score 8; DB 12; Length 204;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
Db 113 RAARAAAR 120

RESULT 10
Q8G2E4 PRELIMINARY; PRT; 274 AA.
ID Q8G2E4
AC Q8G2E4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Chlorophyll A-C binding protein.
OS Pyrocystis lunula.
OC Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.
OX NCBI_TaxID=2972;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamoto O.K., Hastings J.W.;
RA "Circadian oscillations in the transcriptome of dinoflagellate cells:
RT Towards the clock circuitry.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508261; AA014680.1; ..
SQ SEQUENCE 274 AA; 28168 MW; B5F52A5D545AC8BA CRC64;

Query Match 50.0%; Score 8; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
Db 81 AAARRARA 88

RESULT 11
Q9X4X0 PRELIMINARY; PRT; 336 AA.
ID Q9X4X0
AC Q9X4X0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DITH.
GN DITH.
OS Pseudomonas abietaniphila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=89065;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RA Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.;
RA "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin
RT Acids.";
RL Syst. Appl. Microbiol. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RX MEDLINE=99235742; PubMed=10217753;
RA Martin V.J., Mohn W.W.;
RT "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-
RT degrading bacterium Pseudomonas abietaniphila BKME-9.";
RL J. Bacteriol. 181:2675-2682(1999).
DR EMBL; AF119621; AAD21070.1;
DR InterPro: IPR002529; FAA_hydrolase.
DR Pfam; PF01537; FAA_hydrolase; 1.
SQ SEQUENCE 336 AA; 37494 MW; CD221163FB1B44FB CRC64;

Query Match 50.0%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
Db 105 AAARRARA 112

RESULT 12
Q31191 PRELIMINARY; PRT; 356 AA.
ID Q31191
AC Q31191;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MHC class I H2-K gene (Haplotype d) (fragment).
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84170268; PubMed=6143316;
RA Lalanne J.-L., Cochet M., Kummer A.-M., Gachelin G., Kourilsky P.;
RT "Different exon-intron organization at the 5' part of a mouse class I
RT gene is used to generate a novel H-2Kd-related mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565(1983).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).

DR InterPro: IPR004507; Ublx.
DR Pfam: PF02441; Flavoprotein: 1.
DR TIGRFAMs: TIGR00421; ublx: 1.
SQ SEQUENCE 200 AA; 21660 MW; 83D1B5C22C13CD3E CRC64;

Query Match 50.0%; Score 8; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
Db 187 RAARAAAR 194

RESULT 9
Q65545 PRELIMINARY; PRT; 204 AA.
AC Q65545;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE UL3 protein.
GN UL3.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cooper;
RX MEDLINE=96036477; PubMed=7483276;
RA Khattar S.K., van Drunen Littel-van den Hurk S., Babiuk L.A.,
RA Tikoo S.K.;
RT Identification and transcriptional analysis of a 3'-coterminal gene
RT cluster containing UL1, UL2, UL3, and UL3.5 open reading frames of
RT bovine herpesvirus-1.;
RL Virology 213:28-37(1995).
DR EMBL; U32173; AAC54557.1;
DR InterPro: IPR005035; Herpes_UL3.
DR InterPro: IPR005829; Sug. transporter..
DR Pfam; PF03369; Herpes_UL3; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
SQ SEQUENCE 204 AA; 21792 MW; 9292E6A8AA2CB8C6 CRC64;

Query Match 50.0%; Score 8; DB 12; Length 204;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
Db 113 RAARAAAR 120

RESULT 10
Q8G2E4 PRELIMINARY; PRT; 274 AA.
ID Q8G2E4
AC Q8G2E4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Chlorophyll A-C binding protein.
OS Pyrocystis lunula.
OC Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.
OX NCBI_TaxID=2972;
RN [1]
RP SEQUENCE FROM N.A.
RA Okamoto O.K., Hastings J.W.;
RA "Circadian oscillations in the transcriptome of dinoflagellate cells:
RT Towards the clock circuitry.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508261; AA014680.1; ..
SQ SEQUENCE 274 AA; 28168 MW; B5F52A5D545AC8BA CRC64;

Query Match 50.0%; Score 8; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
Db 81 AAARRARA 88

RESULT 11
Q9X4X0 PRELIMINARY; PRT; 336 AA.
ID Q9X4X0
AC Q9X4X0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DITH.
GN DITH.
OS Pseudomonas abietaniphila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=89065;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RA Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.;
RA "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin
RT Acids.";
RL Syst. Appl. Microbiol. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BKME-9;
RX MEDLINE=99235742; PubMed=10217753;
RA Martin V.J., Mohn W.W.;
RT "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-
RT degrading bacterium Pseudomonas abietaniphila BKME-9.";
RL J. Bacteriol. 181:2675-2682(1999).
DR EMBL; AF119621; AAD21070.1;
DR InterPro: IPR002529; FAA_hydrolase.
DR Pfam; PF01537; FAA_hydrolase; 1.
SQ SEQUENCE 336 AA; 37494 MW; CD221163FB1B44FB CRC64;

Query Match 50.0%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
Db 105 AAARRARA 112

RESULT 12
Q31191 PRELIMINARY; PRT; 356 AA.
ID Q31191
AC Q31191;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MHC class I H2-K gene (Haplotype d) (fragment).
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84170268; PubMed=6143316;
RA Lalanne J.-L., Cochet M., Kummer A.-M., Gachelin G., Kourilsky P.;
RT "Different exon-intron organization at the 5' part of a mouse class I
RT gene is used to generate a novel H-2Kd-related mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565(1983).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).

CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).

DR EMBL; K01182; AAA39653.1; -
 DR HSP; P01899; I829.
 DR MGD; MGI:95904; H2-K.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; Igc1; 1.
 DR PROSITE; PS08335; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Glycoprotein; Transmembrane.
 FT NON_TER 356 356
 SQ SEQUENCE 356 AA; 39888 MW; 7BFB4957212E3F2D CRC64;

Query Match 50.0%; Score 8; DB 7; Length 356;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ARAAAR 10
 DB 20 ARAAAR 27
 |||||

RESULT 13

OYI4A1 PRELIMINARY; PRT; 383 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Probable multidrug resistance efflux pump.
 GN PA1237.

OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01;
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goulet L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 408:959-964(2000).
 DR EMBL; AE004533; ANG04626.1; -
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR003997; RTX.
 DR Pfam; PF00529; HlyD; 1.
 DR PRINTS; PR01490; RTXIND.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 42550 MW; 8DE3B490DD83C9B1 CRC64;

Query Match 50.0%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ARAAAR 12
 DB 187 ARAAAR 194
 |||||

RESULT 14

Q8S112

ID Q8S112 PRELIMINARY; PRT; 451 AA.

AC Q8S112;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE P0699H05.2 protein.
 GN P0699H05.2.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0699H05.2";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003299; BAB89880.1; -
 DR Gramene; Q8S112; -
 SQ SEQUENCE 451 AA; 49641 MW; 2E196EAA1DCB1468 CRC64;

Query Match 50.0%; Score 8; DB 10; Length 451;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRAAAR 9
 DB 237 RRAAAR 244
 |||||

RESULT 15

QYI8R0 PRELIMINARY; PRT; 710 AA.

ID QYI8R0;
 AC QYI8R0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ATP-dependent helicase HRPB.
 GN BMEI1818.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE-20020109; PubMed-11756688;
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mueh C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009614; AAL52999.1; -
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW Complete proteome.
 SQ SEQUENCE 710 AA; 76150 MW; 5DCA5720C36DBBFA CRC64;

Query Match 50.0%; Score 8; DB 16; Length 710;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ARAAAR 11
 |||||

Sat Aug 9 19:18:32 2003

us-09-905-691-5.olog.rspt

Page 6

Db 156 AAAAAARR 163

Search completed: August 9, 2003, 16:32:58
Job time : 40.4571 secs